



SEQUENCE LISTING

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The Government of the United States of America
as represented by the Secretary,
Department of Health and Human Services

<120> Pseudomonas Exotoxin A-Like Chimeric Immunogens

<130> 015280-310100US

<140> US 09/462,682

<141> 2000-04-28

<150> US 60/052,375

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<151> 1998-07-10

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1839

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1839)

<223> exotoxin A

<400> 1

gcc	gaa	gaa	gct	ttc	gac	ctc	tgg	aac	gaa	tgc	gcc	aaa	gcc	tgc	gtg	48
Ala	Glu	Glu	Ala	Phe	Asp	Leu	Trp	Asn	Glu	Cys	Ala	Lys	Ala	Cys	Val	
1				5				10						15		

ctc	gac	ctc	aag	gac	ggc	gtg	cgt	tcc	agc	cgc	atg	agc	gtc	gac	ccg	96
Leu	Asp	Leu	Lys	Asp	Gly	Val	Arg	Ser	Ser	Arg	Met	Ser	Val	Asp	Pro	
			20					25						30		

gcc	atc	gcc	gac	acc	aac	ggc	cag	ggc	gtg	ctg	cac	tac	tcc	atg	gtc	144
Ala	Ile	Ala	Asp	Thr	Asn	Gly	Gln	Gly	Val	Leu	His	Tyr	Ser	Met	Val	
			35				40							45		

ctg	gag	ggc	ggc	aac	gac	gcg	ctc	aag	ctg	gcc	atc	gac	aac	gcc	ctc	192
Leu	Glu	Gly	Gly	Asn	Asp	Ala	Leu	Lys	Leu	Ala	Ile	Asp	Asn	Ala	Leu	
	50					55					60					

agc	atc	acc	agc	gac	ggc	ctg	acc	atc	cgc	ctc	gaa	ggc	ggc	gtc	gag	240
Ser	Ile	Thr	Ser	Asp	Gly	Leu	Thr	Ile	Arg	Leu	Glu	Gly	Gly	Val	Glu	
	65				70				75						80	

ccg	aac	aag	ccg	gtg	cgc	tac	agc	tac	acg	cgc	cag	gcg	cgc	ggc	agt	288
Pro	Asn	Lys	Pro	Val	Arg	Tyr	Ser	Tyr	Thr	Arg	Gln	Ala	Arg	Gly	Ser	
				85					90					95		

tgg tgc ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tgc aac	336
Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn	
100 105 110	
atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac	384
Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His	
115 120 125	
atg tgc ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag	432
Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys	
130 135 140	
ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag	480
Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu	
145 150 155 160	
atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg	528
Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met	
165 170 175	
gcc cag acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc	576
Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser	
180 185 190	
ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac	624
Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr	
195 200 205	
ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc	672
Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile	
210 215 220	
tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa	720
Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys	
225 230 235 240	
ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg	768
Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu	
245 250 255	
gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc	816
Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe	
260 265 270	
acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag tgc ggc	864
Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly	
275 280 285	
tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg cgg ctg tgc	912
Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser	
290 295 300	
tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc	960
Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly	
305 310 315 320	
agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc	1008
Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala	
325 330 335	

aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag 1776
 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
 580 585 590

gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg 1824
 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
 595 600 605

cgc gag gac ctg aag 1839
 Arg Glu Asp Leu Lys
 610

<210> 2

<211> 613

<212> PRT

<213> Pseudomonas aeruginosa

<400> 2

Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
 1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
 20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
 35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
 50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
 65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
 85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
 100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
 115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
 130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
 145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
 165 170 175

Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
 180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
 195 200 205

Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
 210 215 220

Tyr	Arg	Val	Leu	Ala	Gly	Asn	Pro	Ala	Lys	His	Asp	Leu	Asp	Ile	Lys	225	230	235	240
Pro	Thr	Val	Ile	Ser	His	Arg	Leu	His	Phe	Pro	Glu	Gly	Gly	Ser	Leu	245	250	255	
Ala	Ala	Leu	Thr	Ala	His	Gln	Ala	Cys	His	Leu	Pro	Leu	Glu	Thr	Phe	260	265	270	
Thr	Arg	His	Arg	Gln	Pro	Arg	Gly	Trp	Glu	Gln	Leu	Glu	Gln	Cys	Gly	275	280	285	
Tyr	Pro	Val	Gln	Arg	Leu	Val	Ala	Leu	Tyr	Leu	Ala	Ala	Arg	Leu	Ser	290	295	300	
Trp	Asn	Gln	Val	Asp	Gln	Val	Ile	Arg	Asn	Ala	Leu	Ala	Ser	Pro	Gly	305	310	315	320
Ser	Gly	Gly	Asp	Leu	Gly	Glu	Ala	Ile	Arg	Glu	Gln	Pro	Glu	Gln	Ala	325	330	335	
Arg	Leu	Ala	Leu	Thr	Leu	Ala	Ala	Ala	Glu	Ser	Glu	Arg	Phe	Val	Arg	340	345	350	
Gln	Gly	Thr	Gly	Asn	Asp	Glu	Ala	Gly	Ala	Ala	Asn	Ala	Asp	Val	Val	355	360	365	
Ser	Leu	Thr	Cys	Pro	Val	Ala	Ala	Gly	Glu	Cys	Ala	Gly	Pro	Ala	Asp	370	375	380	
Ser	Gly	Asp	Ala	Leu	Leu	Glu	Arg	Asn	Tyr	Pro	Thr	Gly	Ala	Glu	Phe	385	390	395	400
Leu	Gly	Asp	Gly	Gly	Asp	Val	Ser	Phe	Ser	Thr	Arg	Gly	Thr	Gln	Asn	405	410	415	
Trp	Thr	Val	Glu	Arg	Leu	Leu	Gln	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	420	425	430	
Gly	Tyr	Val	Phe	Val	Gly	Tyr	His	Gly	Thr	Phe	Leu	Glu	Ala	Ala	Gln	435	440	445	
Ser	Ile	Val	Phe	Gly	Gly	Val	Arg	Ala	Arg	Ser	Gln	Asp	Leu	Asp	Ala	450	455	460	
Ile	Trp	Arg	Gly	Phe	Tyr	Ile	Ala	Gly	Asp	Pro	Ala	Leu	Ala	Tyr	Gly	465	470	475	480
Tyr	Ala	Gln	Asp	Gln	Glu	Pro	Asp	Ala	Arg	Gly	Arg	Ile	Arg	Asn	Gly	485	490	495	
Ala	Leu	Leu	Arg	Val	Tyr	Val	Pro	Arg	Ser	Ser	Leu	Pro	Gly	Phe	Tyr	500	505	510	
Arg	Thr	Ser	Leu	Thr	Leu	Ala	Ala	Pro	Glu	Ala	Ala	Gly	Glu	Val	Glu	515	520	525	
Arg	Leu	Ile	Gly	His	Pro	Leu	Pro	Leu	Arg	Leu	Asp	Ala	Ile	Thr	Gly	530	535	540	

Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
 545 550 555 560

Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
 565 570 575

Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
 580 585 590

Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
 595 600 605

Arg Glu Asp Leu Lys
 610

<210> 3
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus type 1

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> V3 loop of MN strain of HIV-1

<400> 3
 Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro
 1 5 10 15

Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln
 20 25 30

Ala His Cys
 35

<210> 4
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus type 1

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> V3 loop of Thai-E strain of HIV-1

<400> 4
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro
 1 5 10 15

Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp Ile Arg Lys
 20 25 30

Ala Tyr Cys
 35

<210> 5
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: coding strand
 of duplex containing novel PstI site

<400> 5
 tggccctgac cctggccgcc gccgagagcg agcgcttcgt ccggcagggc accggcaacg 60
 acgaggccgg cgcggaacac ctgcagggcc 90

<210> 6
 <211> 24
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Ib loop region of wild-type Pseudomonas exotoxin A

<400> 6
 Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala
 1 5 10 15

Gly Glu Cys Ala Gly Pro Ala Asp
 20

<210> 7
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ib loop region
 of ntPE-V34MN14 protein

<400> 7
 Gly Ala Ala Asn Leu His Cys Gly Ile His Ile Gly Pro Gly Arg Ala
 1 5 10 15

Phe Tyr Thr Thr Lys Cys Met Gln Gly Pro Ala Asp
 20 25

<210> 8
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ib loop region
 of ntPE-V3MN26 protein

<400> 8
 Gly Ala Ala Asn Leu His Cys Asn Tyr Asn Lys Arg Lys Arg Ile His
 1 5 10 15

Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr
 20 25 30

Ile Cys Met Gln Gly Pro Ala Asp
 35 40

<210> 9
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ib loop region
 of ntPE-V3Th-E26 protein

<400> 9
 Gly Ala Ala Asn Leu His Cys Ser Asn Asn Thr Arg Thr Ser Ile Thr
 1 5 10 15

Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp
 20 25 30

Asp Ile Cys Met Gln Gly Pro Ala Asp
 35 40

<210> 10
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ib loop region
 of ntPE-fp16 protein

<400> 10
 Gly Ala Ala Asn Leu Gln Cys Arg Leu Glu Glu Lys Lys Gly Asn Tyr
 1 5 10 15

Val Val Thr Asp His Arg Leu Cys Leu Gln Gly Pro Ala Asp
 20 25 30

<210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:endoplasmic
 reticulum (ER) retention sequence

<400> 11
 Arg Glu Asp Leu Lys
 1 5

<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 12
Arg Glu Asp Leu
1

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 13
Lys Asp Glu Leu
1